

1PEA/US

FIG. 1

736-747 (E0)

779-781 (E0)

RPOC_ECOLI (725)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_HAEIN (726)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_VIBCH (726)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_PSEAE (726)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_TREPA (682)	NATSGARGSRND	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_BORBU (688)	NADSGARGSRND	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_XYLEA (748)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_CAMJE (723)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_NEIMA (727)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_RICPR (719)	NATSGARGST	QIKOLGAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_CHLIR (725)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_MAYCPN (809)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_BACSU (728)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_STAAU (733)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_MYCTU (802)	IVDSGATGNT	TYRDLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_SYNY3 (752)	NADSGARGSAA	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_AQUAE (839)	NATSGARGSRND	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_DEIRA (1041)	MSQSGARGSPQ	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_ITHER (1023)	MAQSGARGSPQ	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPOC_THEAG (1023)	MAQSGARGSPQ	DIROLAAGHRLM	KPDGS	IIETP	ITAMF REGLVNQYF	IS THGARK	ELADTALKTA	DAG YLTPRL
RPAL_HUMAN (887)	NVQSGAKGSTY	WTWQISCLLGO	IEL EGRSTPLMA3	-----	6KSLPCPEP	PEPTFRAGG	FTVGRFTG	IKPPEPFFCHVA
RPBI_HUMAN (788)	MYVSGAKGSK	IIHISQV	IADVCGQV	VEGRIRPFGK	-----	HRTLPPIEDDY	GRHSRGFTVDS	VLACLTPTPTFHANG
RPCI_HUMAN (780)	MAICUSKGSF	IIHISQV	IADVCGQV	VEGRIRPFGK	-----	HRTLPPIEDDY	GRHSRGFTVDS	VLACLTPTPTFHANG

BACTERIAL RNA
POLYMERASE

HUMAN RNA
POLYMERASES
I, II, III

10/526323

PCT/US03/27457.16092004

2/5

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FIG. 2

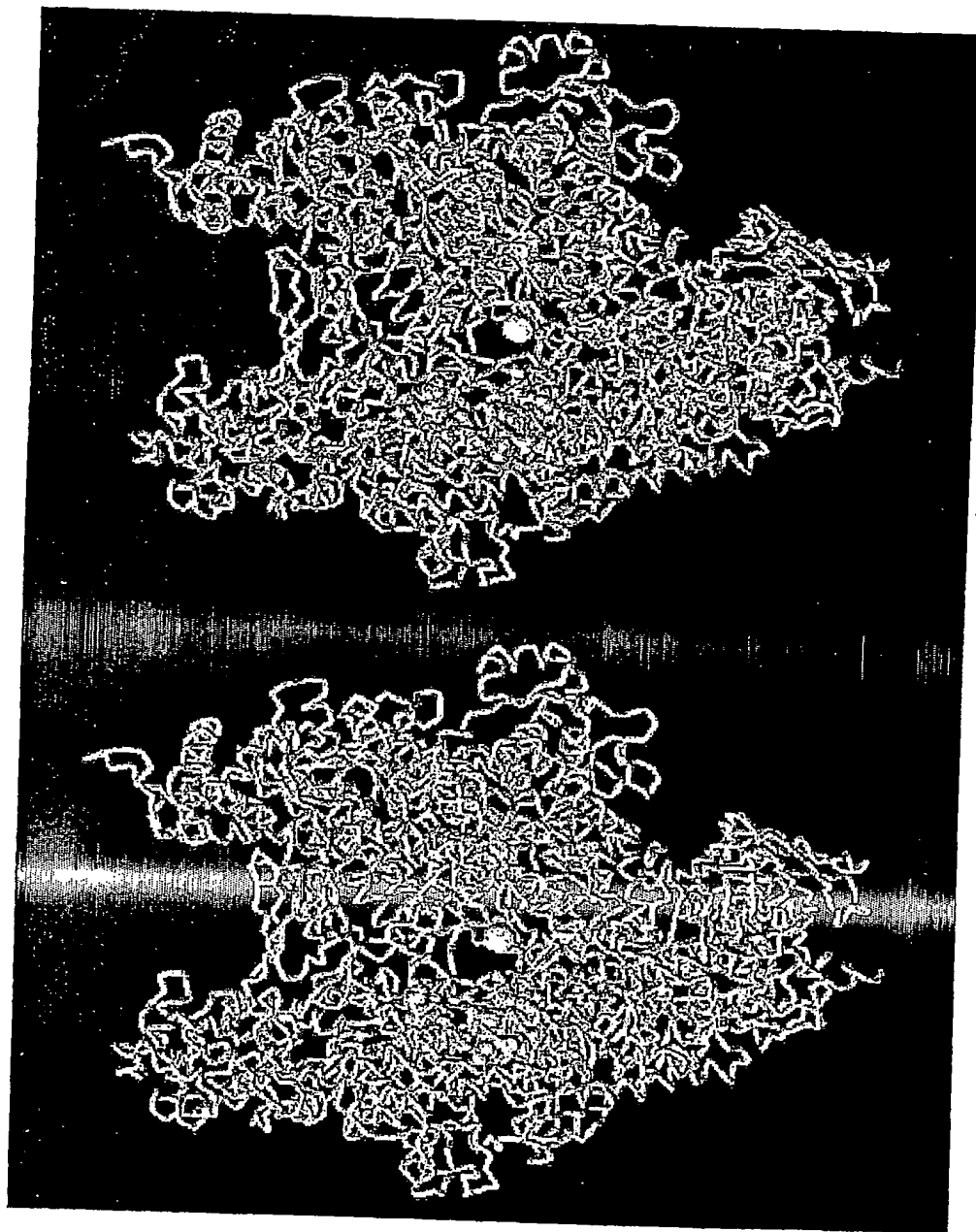


FIG. 3

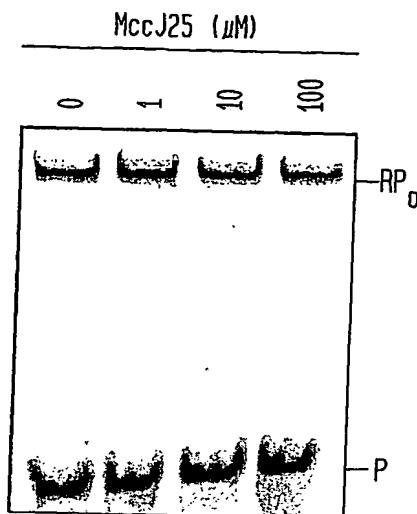


FIG. 4A

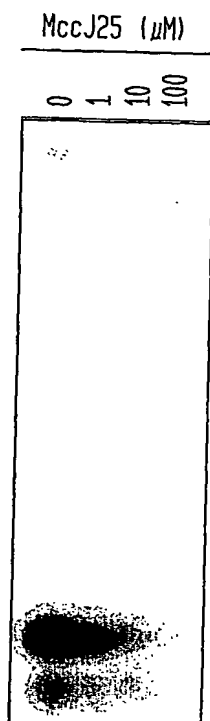


FIG. 4B

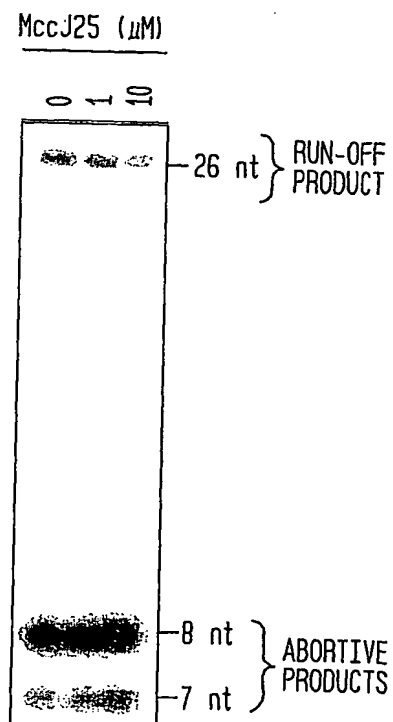


FIG. 5A

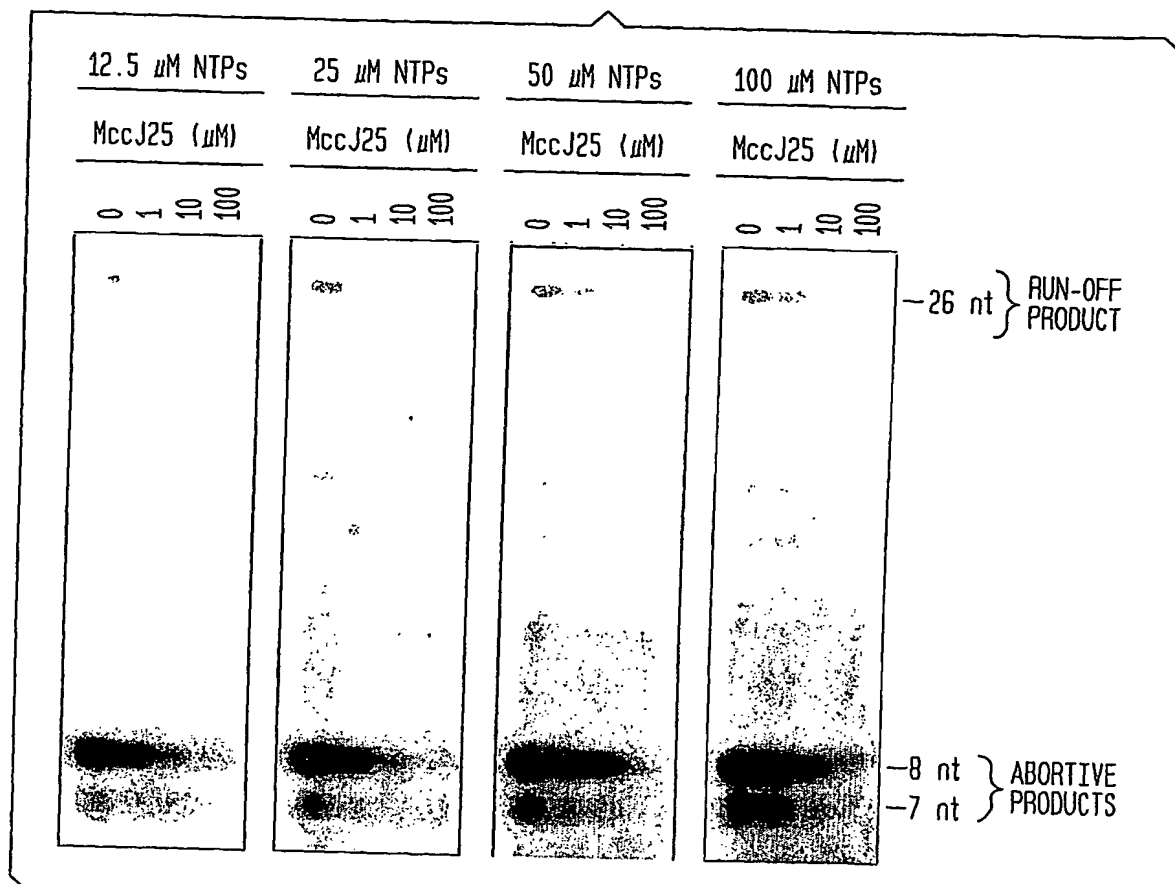


FIG. 5B

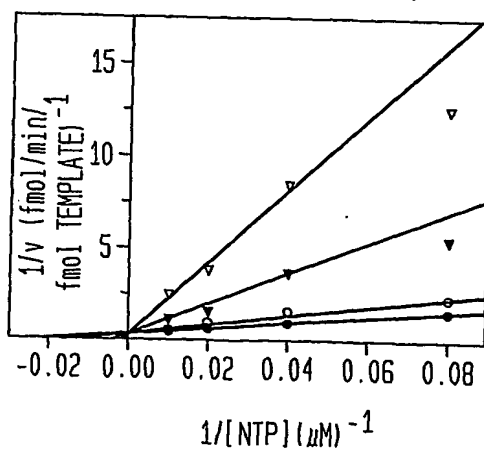


FIG. 5C

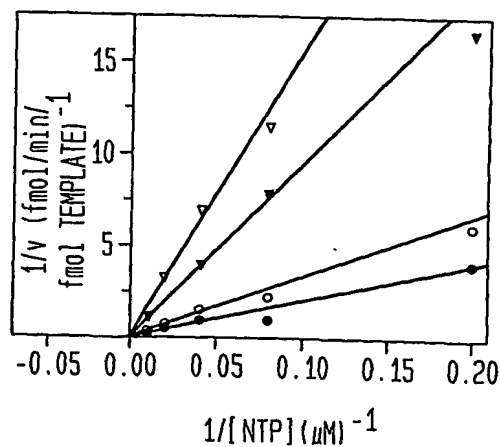


FIG. 6A

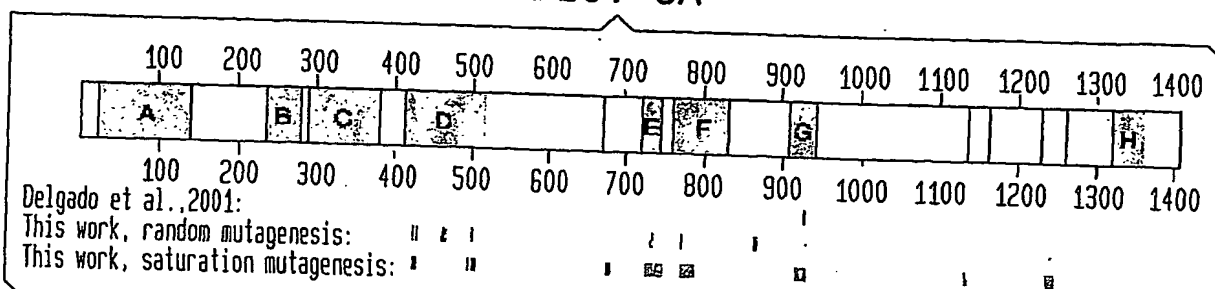


FIG. 6B

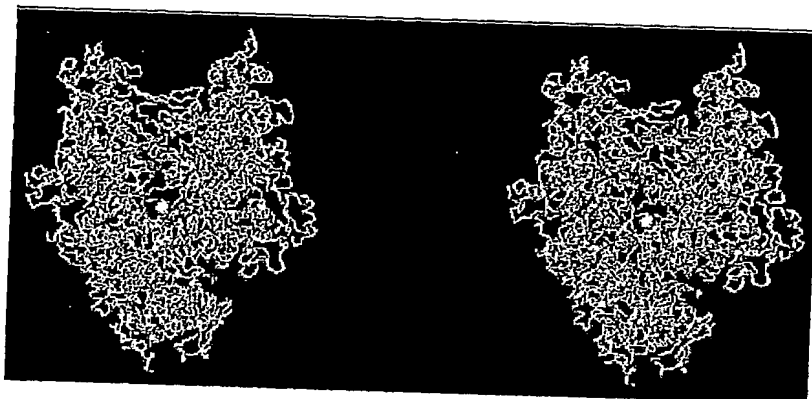


FIG. 6C

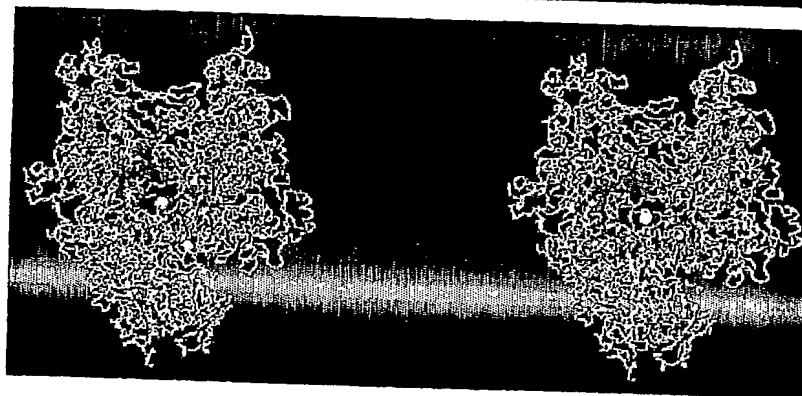


FIG. 6D

